

to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. U.S.A. 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

IN THE CLAIMS

Please amend claims 1, 2, 4, 9, 13 and 30, and add new claims 38-40. Claims not amended or new are reiterated for the Examiner's convenience.

1. **(twice amended)** An isolated cadherin-like asymmetry protein-5 (CLASP-5) polynucleotide, wherein said polynucleotide encodes at least 20 contiguous amino acids of SEQ ID NO:2 or a biologically active variant thereof;
2. **(amended)** The polynucleotide of claim 1, wherein said polynucleotide encodes at least 20 contiguous amino acids of SEQ ID NO:2 or an allelic variant thereof.
3. **(reiterated)** The isolated polynucleotide of claim 1, comprising the cDNA coding sequence of ATCC accession numbers PTA-1565, PTA-1568, PTA-2609 or PTA-2612.
4. **(amended)** An isolated CLASP-5 polynucleotide comprising a nucleotide sequence that has at least 90% percent identity to SEQ ID NO:1.
6. **(reiterated)** A vector comprising the polynucleotide of claim 1,

expression of the polynucleotide in a host cell.

8. **(reiterated)** A host cell comprising the polynucleotide of claim 1, or progeny of the cell.

9. **(amended)** A host cell comprising the polynucleotide of claim 1, wherein the nucleotide sequence of the polynucleotide is operably linked with a regulatory sequence that controls expression of the polynucleotide in a host cell, or progeny of the cell.

10. **(reiterated)** The host cell of claim 8 which is a eukaryote.

11. **(reiterated)** The polynucleotide of claim 1 that is an antisense polynucleotide less than about 200 bases in length.

12. **(reiterated)** An antisense oligonucleotide complementary to a messenger RNA comprising SEQ ID NO: 1 and encoding CLASP-5, wherein the oligonucleotide inhibits the expression of CLASP-5.

13. **(amended)** An isolated CLASP-5 polynucleotide comprising at least 50 contiguous nucleotides of SEQ ID NO:1.

14. **(reiterated)** The polynucleotide of claim 1 that is RNA.

15. **(reiterated)** A method for producing a polypeptide comprising:

- (a) culturing the host cell of claim 8 under conditions such that the polypeptide is expressed; and
- (b) recovering the polypeptide from the cultured host cell or its cultured medium.

30. **(amended)** A composition comprising a polynucleotide of claim 1 and a carrier.

38. **(new)** The polynucleotide of claim 1, wherein said polynucleotide encodes a polypeptide having at least 20 contiguous amino acids of SEQ ID NO:2

(new) A method for identifying a polynucleotide that encodes a polypeptide having at least 20 contiguous amino acids of SEQ ID NO:1 under conditions of high stringency.

40. **(new)** An isolated CLASP-5 polynucleotide, wherein said polynucleotide encodes a polypeptide having 95% or more sequence identity with SEQ ID NO:2.